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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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17
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  184.5
182
173
173
170
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163.5
163.1
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                                                                                                                             200
193
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1733
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         425026 seqs, 132305027 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
                                                                                                                                                                                                                                                                                                                                        sp_phage: *
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sp_bacteria:*
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sp_vertebrate:*
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sp_rodent:*
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 239
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(without alignments)
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060592 homo
Q9uft2 homo
                       060593 homo sapien
060592 homo sapien
Q9uft2 homo sapien
042287 xenopus lae
035413 rattus norv
09p7e8 schizosacch
Q9y338 homo sapien
09p290 homo sapien
                                     Q9p7e8
Q9y338
                                                                                                                                     Q9pull xenopus lae
Q9ve96 drosophila
                 Q9p2q0 homo sapien
Q9wve9 rattus norv
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                                                                                                         Q9u2t9
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Q9yhu7 xenopus lae
Q9u2t9 caenorhabdi
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Q99059 avian
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59 avian sarco
3 caenorhabdi
drosophila
drosophila
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8.7	8.7	8.7				8.8				8.9	8.9	9.0.	9.0	9.0	9.1	9.1	9.1	9.1	9.1	9.1				9.2	
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Q9QY53	061080	Q9WVE1	Q9TYT3	097180	061639	Q9Z0R4	075815	Q9Z0Z9	Q9Z0Z8	Q62417	097337	Q24145	Q9V5J3	Q9NRB7	Q9NZM3	Q9NYG0	Q9ULG4	Q9NZM2	Q9QZK2	Q9UNK1	Q9UHN7	Q9UNK2	Q9UET5	095216	094875
Q9qy53 mus musculu	061080 acanthamoeb	Q9wvel rattus norv	Q9tyt3 caenorhabdi		061639 drosophila	Q9z0r4 mus musculu	075815 homo sapien	Q9z0z9 mus musculu	Q9z0z8 mus musculu	Q62417 mus musculu	097337 paracentrot		Q9v5j3 drosophila	Q9nrb7 homo sapien	homo	homo	homo	homo	Q9qzk2 mus musculu	Q9unk1 homo sapien	Q9uhn7 homo sapien	Q9unk2 homo sapien	Q9uet5 homo sapien	095216 homo sapien	094875 homo sapien

ALIGNMENTS

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RESULT
Q9QW60
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                                                                                               Query Match
Best Local Similarity
Matches 206; Conserv
                                                                                                                                                                          Pfam; PF00017; SH2; 1.
Pfam; PF00018; SH3; 1.
PRINTS; PR00401; SH2; DMAIN.
PRINTS; PR00452; SH3DOMAIN.
PROSITE; PS50001; SH2; 1.
PROSITE; PS50002; SH3; 1.
SMART; SM00326; SH3; 1.
SEQUENCE 239 AA; 26013 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9QW60 PRELIMINARY;
Q9QW60;
Q1-MAY-2000 (TrEMBLrel. 13,
Q1-MAY-2000 (TrEMBLrel. 13,
Q1-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                          Margolis B., Silvennoinen O., Comoglio F., Roonprapunt C., Skolnik E., Willrich A., Schlessinger J.;
"High-efficiency expression/cloning of epidermal growth factor-receptor-binding proteins with Src homology 2 domains.";
Proc. Natl. Acad. Sci. U.S.A. 89:8894-8898(1992).
HSSP; Q64010; ICKA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
GRB-3-EPIDERMAL GROWTH FACTOR-RECEPTOR-BINDING PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE=93028373; PubMed=1409582;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10095;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus sp
                                                                                                                                                                                                                                                                                                           InterPro; IPR000980; -.
InterPro; IPR001452; -.
65 INSSGPRPPVPPSPAQPPPGVSPSRLRIGDQEFDSLPALLEFYKIHYLDTTTLIEPVARS
                                  \omega
                                                                u
                                                   AGNFDSEERSSWYWGRLSRQEAVALLQGQRHGVFLVRDSSTSPGDYVLSVSENSRVSHYI
                                  AGNFDSEERSSWYWGRLSRQEAVALLQGQRDGVFLVRDSSTSPGDYVLSVSENSRVSHYI
                                                                                                 Conservative
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                                                                                                            62.2%;
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                                                                                               Score 1078; DB 11;
Pred. No. 1.7e-81;
0; Mismatches 1;
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Best Local Similarity
Matches 159; Conserv
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MEDLINE-90045469; PubMed-2554234;
TSuchie H., Chang C.H.W., Yoshida M., Vo
"A newly isolated avian sarcoma virus, A
oncogene.";
Oncogene 4:1281-1284(1989).
-! - SIMILARITY: CONTAINS A COPY EACH OF
EMBL; X17292; CAA35181.1; -.
HSSP: 064010; 1CKA.
                                                                                                                                                                                                      DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q99059;
01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                               Oncogene;
NON_TER
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Pfam; PF00018; SH3; 1.
PFINTS; PR00401; SH2DOMAIN.
PRINTS; PR00452; SH3DOMAIN.
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                                                                                                                                                                                                                                                                                 SMART;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAG-CRK PROTEIN (FRAGMENT).
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 232
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                                                                                    INSSGPRPPVPPSPAQP-PPGVSPSRLRIGDQEFDSLPALLEFYKIHYLDTTTLIEPVAR 123
                                                                                                                            AGNFDSEERSSWYWGRLSRQEAVALLQGQRHGVFLVRDSSTSPGDYVLSVSENSRVSHYI 64
MIPVPYVEKCRPSSASVSTLTGG
           MIPVPYVEKYRPASASVSALIGG
                                               SRQGSGVILRQEEAEYVRALFDFNGNDEEDLPFKKGDILRIRDKPEEQWWNAEDSEGKRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SRQNSGVILRQEEVEYVRALFDFNGNDDEDLPFKKGDILKIRDKPEEQWWNAEDMDGKRG
                                                                           VNSLGPAGGRRAGGEGPGAPGLNPTRFRIGDQEFDSLLEFYKIHYLDTTTLIEPVSR
                                                                                                                  AGQFDSEDRGSWYWGRLSRGDAVSLLQRERHGTFLVRDSGSIPGDFVLSVSESSRVSHYI
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                                                                                                                                                                                                                                                                                 SM00326;
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24
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188
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255
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Pred. No. 2.5e
17; Mismatches
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                                                                                                                                                                                                   GAG (BY SIMILARITY).
CRK (BY SIMILARITY).
SH2 (OR B+C BOX) (BY SIMILARITY).
SH3 (OR A BOX) (BY SIMILARITY).
GAG (BY SIMILARITY).
; 0C562D0B2327A579 CRC64;
                  206
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No. 2.
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, ASV-1, carries
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Best Loc
Matches
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Q9PU11;
Q1-MAY-2000
Q1-MAY-2000
Q1-MAR-2001
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Q9NHC3;
Q9NHC3;
01-OCT-2000
01-OCT-2000
01-MAR-2001
                                                        Xenopus laevis (African clawed frog).
Bukaryota; Metazoa; Chordata; Craniata; Ve.
Amphibia; Batrachia; Anura; Mesobatrachia;
Xenopodinae; Xenopus.
NCBI_TaxID=8355;
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Nat. Cell Biol. 0:0-0(2000)
EMBL; AF226866; AAF33845.1;
  SEQUENCE FROM N.A. Goisset C., Shi D.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PRO0401; SH2DOMAIN.
PRINTS; PR00452; SH3DOMAIN.
PROSITE; PS50001; SH2; 1.
PROSITE; PS50002; SH3; 1.
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InterPro; IPR001452;
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Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
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Similarity 31.0%;
93; Conservative !
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                                                                                                                                                                                                             0 (TrEMBLrel. 13, 0 (TrEMBLrel. 13, 11) (TrEMBLrel. 16,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence up
(TrEMBLrel. 16, Last annotation
ENGULEMENT PROTEIN CED-2.
                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Horvitz H.R.;
and CED-10/Rac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nematoda; Chromadorea; rinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30878 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----EDGTAAAGVKIANQSFPDIPALLNHFKMRVLTEASLL---
    Boucaut J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52;
                                                                                                                                                                                                               Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  control
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 343; DB 5;
Pred. No. 1.2e-20;
2; Mismatches 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----KGASQSSIGSSGGGAERFSSASTSSDNIEL
                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5CE7DA478948970B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  phagocytosis
                                                                                                                                                                                                                                                                                                    217
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                                                                                                        Vertebrata;
.a; Pipoidea;
                                                                                                                                                                                                                                                                                                  æ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rhabditida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          111;
                                                                                                                                                                                                               update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 279;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                        Euteleostomi;
Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     migration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44;
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                                                                                                                                                                                                                                                                                                                                                                                                        273
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RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA Amanatides P.G., Scherer S.E., Richards S., Ashburner M., Henderson S.N.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA George R.A., Lewis S.E., Richards S., Nalang Q., Chen L.X.,

RA George R.A., Lewis S.E., Richards S., Nelson C.R., Miklos G.L.G.,

RA Hardon R.C., Rogers Y.-H.C., Blaze'J R.G., Champe M., Pfeiffer B.D.,

RA Hardon R.C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Baltew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Bavokstein P., Brottier P.,

RA Borkova D., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Ferriar S., Fleischmann W.,

RA Durbin K.J., Evangelista C.C., Ferriar C., Ferriera S., Fleischmann W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PRO0499; P67PHOX.
PRINTS; PRO0401; SH2DOMAIN.
PRINTS; PRO0452; SH3DOMAIN.
PROSITE; PS50001; SH2; 1.
PROSITE; PS50002; SH3; 2.
SMART; SM00326; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9VE96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            by interfering mutants of Sem-
Submitted (DEC-1997) to the EM
EMBL; AJC23061; CAB59279.1; -.
HSSP; P29354; 1GHU.
                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ptam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000108; -.
InterPro; IPR000980; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CG7129 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Selective inhibition of neural induction but not mesoderm induction by interfering mutants of Sem-5/Grb2.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KRGMIPVPYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q---IFLRDIEQVPQQPTYVQALFDFDPQEDGELGFRRGDFIQVVDNSDPNWWKG-TCLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QGSGVILRQ-----EEAEYVRALFDFNGNDEEDLPFKKGDILRIRDKPEEQWWNAEDSEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NSSGPRPPVPPSPAQPPPGVSPSRLRIGDQEFDSLPALLEFYKIHYLDTTTLIEPVARSR 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NYIEMKAHPWFFGKIPRAKAEEMLGKORHDGAFLIRESESAPGDFSLSVKFGNDVQHFKV 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NFDSEERSSWYWGRLSRQEAVALLQGQRH-GVFLVRDSSTSPGDYVLSVSENSRVSHYII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PF00017; SH2; 1. PF00018; SH3; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SM00326;
ICE 217 /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         l Similarity 27.4
52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR001452; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                      N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25135 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----AGKYFLWVVKFNSLNELVDYHR----STS----VSRNQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13,
16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 213; DB 13;
Pred. No. 4.9e-10;
5; Mismatches 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2349A68260F9D4CD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                               Miklos G.L.G.,
    Baldwin D.,
easley E.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      65
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RESULT
Q9YHUG
ID QS
AC QS
AC QS
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DT 01
DT 01
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RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA McIntosh T.G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA McIntosh T.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Shue B.C., Siden-Kiamos I., Sanders R.D.C., Scheelaer F., Shen H.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Sylrskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Yeb R., F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
Stence 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                             Q9YHU6:

Q9YHU6:

O1-MAY-1999 (TrEMBLrel. 10, Created)
O1-MAY-1999 (TrEMBLrel. 16, Last sequ
O1-MAY-2001 (TrEMBLrel. 16, Last anno
PHOSPHOLIPASE C-GAMMA-1B (FRAMENT)
Xenopus laevis (African clawed freq).
                Eukaryota; Metazoa; Chordata; Craniata;
Amphibia; Batrachia; Anura; Mesobatrachi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00499; P67PHOX. PRINTS; PR00452; SH3DOMAIN. PROSITE; PS50002; SH3; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS5000;
SMART; SM00326;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE003721; AAF55531.1; -. HSSP; P29354; IGFC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FlyBase; FBgn0038599; CG7129
 Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001452;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000108;
                                                                                                                                                                                                                                            587
                                                                                                                                                                                                                                                                             292
                                                                                                                                                                                                                                                                                                                                               241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     THVRLLDQ
                                                                                                                                                                                                                                                                                                                                                                                                                   KRGMIPVPYVEKYRPASASVSALIGGNQEGSHPQPLGGPEPGPYAQPSVNTPLPNLQNGP
                                                                                                                                                                                                                                                                                                                                                                                  CEGIFPINYVDIKVPLGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                    LSNGCQG ---YMEEEVVPYAVALYDFDGTEPGDLSFREGEKIYLLDHPTPEWLRGRTRSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGYAGSETPPSPPMPKGPPPPPPPASSGGISLLDVINGKVDAL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SHYIINSSGPRPPVPPSPAQPPPGVSPSRLRIGDQEFDSLPALLEFYKIHYLDTTTLIEP 120
                                                                                                                                                                                                                                          --ANFLDQ
                                                                                                                                                                                                                                                                                                                                               TYARVIQKRVPNAY - - - - - - - - DKTALALEVGELVKVTKINVSGQW-EGECNGKRGHFPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PF00018; SH3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             600 AA;
                                                                                                                                                                                                                                                                                                              QQQLPTALCLYHFPGEVEGDLALQENELVTVL-YRINEDWLYGEVAGRQGQFP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                             299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SH3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62961 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35;
                                                                                  Last sequence up
                Mesobatrachia; Pipoidea;
                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 200;
Pred. No. 2
                                                     frog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9E3EA36CC4A165A3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                  Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 5;
.2e-08;
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                                                                                                                                                                                                                                                                                                                                                                                  GGAAAAPTASAAAPSPSPS----
                                                                                                      update)
                                                                                    update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                  Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            60;
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                                                                                                                                                                                                                                                                                                                                                                                  534
                                                                                                                                                                                                                                                                                                                                                                                                                   240
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PRO0390; PHPHLIPASEC.
PRINTS; PRO0401; SH2DOMAIN.
PRINTS; PRO0401; SH2DOMAIN.
PROWITE; PRO0402; SH3DOMAIN.
PROSITE; PS50004; C2_DOMAIN.; UNKNOWN_1.
PROSITE; PS50003; PH_DOMAIN; 1.
PROSITE; PS50007; PIPLC_X_DOMAIN; 1.
PROSITE; PS50007; PIPLC_X_DOMAIN; 1.
PROSITE; PS500007; PIPLC_X_DOMAIN; 1.
PROSITE; PS50001; SH2; 2.
PROSITE; PS50001; SH2; 2.
PROSITE; PS50002; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gamma-1.";
Submitted (SEP-1998)
EMBL; AF090112; AAD03
HSSP; P08487; 2PLD.
                                                                                                                                                                                                                                                                                                                                                                                     NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00387; PI-PLC-Y; 1. Pfam; PF00388; PI-PLC-X; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kung H.-F., Kim J., Huang
"Molecular cloning of two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=8355;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                         122
           254
                                                    207
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                                                                                               169
                                                                                                                     636
                                                                                                                                                              576
                                                                                                                                                                                                       516
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                                                                                                                                                                                                                                                                                        396 GSQANDDEEEQKEASNSSELHSAEKWFHGKLGAGRDGRHIAERLLTDYCIETGAPDGSFL 455
                                                                                                                                                                                  92
                                                                                                                                                                                                                                                                   40
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                                                                                                                                                                                                                                             VRESETFVGDYTLSFWRNGKVQHCRIHSRQEAGSPKLLLTDNLVFESLYALITHYQQMPL 515
                                                                                                                                                                                                                                                                   VRDSSTSPGDYVLSVSENSRVSHYIINS----SGPR-------
                                                                                                                               ARSRQGSGVILRQEEAEY------VRALFDFNGNDEEDLPFKKGDILRIRDKP 168
                                                                                                                                                                                                                                                                                                            GCAGNFDSEER-----SSWYWGRL----SRQEAVALL-----QGQRHGVFL 39
---YDKTALALEVGELV
                              APRQDVHNGRPFVFTITGPQLNRYPLDVAADTLEDMQD---WIRKIREAAQTADARLTEG
                                                                                             EEQWWNAEDSEGKRGM-IPVPYVEK-YRPA------
                                                                                                                  GTPDPDYGALYEGRNPGFYVEANPMPTFKCSVRALFDYKAQREDELTFTKNTIIQNVEKQ 695
                                                                                                                                                           SFRAEGKIKHCRVIQEGQSVVLGSSEFDSLVDLISYYEKHPMYRKMKLRYPINEETLEKI 635
                                                                                                                                                                                                                          ------PPVPPSPAQ-----
                                                   --NQEGSHPQP----LGGPEPGPYAQPSVNTPLPNLQNGPIYARVIQKRVPNA---
                                                                         EGGWWRG-DCGGKKQMWFPANYVEEIFSPAEPEPERQNLDENSPLGDLLGGVLDVPSCHI
                                                                                                                                                                                                      RCNEFEMRLTEPVPQTNAHESKEWYHASLTRGQAEHMLMRVPRDGAFLVRKRSEQNSYAI 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PF00018;
                                                                                                                                                                                                                                                                                                                                                                                                                     SM00239;
                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1067 AA;
                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     C2; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1998) to the EMBL/GenBank/DDBJ databases AAD03595.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                 1067
                                                                                                                                                                                                                                                                                                                                            11.18; 21.78;
                                                                                                                                                                                                                                                                                                                                                                                     124019 MW;
                                                                                                                                                                                 ---IGDQEFDSLPALLEFY-----KIHYLDTTTLIEPV 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               different
                                                                                                                                                                                                                                                                                                                                  43;
                                                                                                                                                                                                                                                                                                                                          Score 193; DB 13;
Pred. No. 1.8e-07;
                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                     533F6876ECDFE5DB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                M.C.;
                                                                                                                                                                                                                          -----PPPGVSPSRLR-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of Xenopus phospholipase
                                                                                                                                                                                                                                                                                                                                  123;
                                                                                            -SASVSALIGG-----
                                                                                                                                                                                                                                                                                                                                                    Length 1067;
                                                                                                                                                                                                                                                                                                                                  Indels 176;
                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                   71
                               811
                                                                       754
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Best Local Similarity
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PÉAM; PF00388; PI-PLC-Y; 1.
PFAM; PF00388; PI-PLC-X; 1.
PRINTS; PR00390; PHPHLIPASEC.
PRINTS; PR00401; SH2DOMAIN.
PRINTS; PR00401; SH2DOMAIN.
PRNITS; PR00452; SH3DOMAIN.
PROSITE; PS50004; C2_DOMAIN.2; 1.
PROSITE; PS50007; PIPLC_X_DOMAIN; 1
PROSITE; PS50008; PIPLC_X_DOMAIN; 1
PROSITE; PS50001; SH2; 2.
PROSITE; PS50001; SH2; 2.
PROSITE; PS50001; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00017; SH2; 2
Pfam; PF00018; SH3; 1
Pfam; PF00168; C2; 1.
Pfam; PF00169; PH; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9YHU7
Q9YHU7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
PHOSPHOLIPASE C-GAMMA-1A (FRAGMENT).
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gamma-1.";
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF090111; AAD03594.1; HSSP; P08487; 2PLD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
Kung H.-F., Kim J., Huang
"Molecular cloning of two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
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                                                                                                                                                                                            378
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                                                                                                438
498 SFRAEGKIKHCRVIQEGQSVVLGSSEFDSLVDLISYYEKHPLYRKMKLRYPINEETLEKI
                                                                                                                                                                                                                                                                                          318 GNQANDDEEEQKEASNSSELHSAEKWFHGKLGAGRDGRHIAERLLTDYCIETGAPDGSFL
                                                                                                                                                 72
                                                                                                                                                                                                                     3 GCAGNFDSEER-----SSWYWGRL----SRQEAVALL-----QGQRHGVFL
                                                                                                                                                                                            VRESETFVGDYTLSFWRNGKVQHCRIHSRQEAGSPKFFLTDNLVFESLYALITHYQQMPL
                                                                                              RCNEFEMRLTEPVPQTNAHESKEWYHASLTRGQAEHMLMRVPRDGAFLVRKRSEQNSYAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SM00252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | IPRO000008 | ... | IPRO000008 | ... | IPRO000009 | ... | IPRO001000 | ... | IPRO011000 | ... | IPRO011000 | ... | IPRO01720 | ... | IPRO01720 | ... | IPRO01849 | ... | IPRO
                                                                                                                                              -----PPVPPSPAQ-----
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1010 AA;
                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SH2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1010
                                                                                                                                                                                                                                                                                                                                                                                                               10.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           116693 MW;
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different
                                                IGDQEFDSLPALLEFY --
                                                                                                                                                                                                                                                                                                                                                                                        28;
                                                                                                                                                                                                                                                                                                                                                                                                               Score 184.5; DB 1
Pred. No. 8.5e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                        Mismatches 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           213247F73EE3EEDA CRC64;
                                                                                                                                              M.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1010
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                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 13;
                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                -KIHYLDTTTLIEPV 121
                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1010;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Euteleostom1;
; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         phospholipase
                                                                                                                                                                                                                                                                                                                                                                                      161;
                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                              437
                                                                                                497
                                                                                                                                                                                                                                                                                             377
                                                                                                                                                                                                                                                                                                                                           39
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Best L
                                                                                                                                       Matches
                                                                                                                                                                                                                 Pfam; PF00018; SH3; 5.
Pfam; PF00036; efhand; 2.
PRINTS; PR00499; P67PHOX.
PRINTS; PR00452; SH3DOMAIN.
PROSITE; PS00152; ATPASE ALPHA BETA; UN PROSITE; PS00018; EF_HAND; UNKNOWN_2.
PROSITE; PS000018; EF_HAND; UNKNOWN_2.
SMART; SM00054; EFh; 1.
                                                                                                                                                                                                                                                                                                             InterPro; IPR000108; -.
InterPro; IPR000194; -.
InterPro; IPR000261; -.
InterPro; IPR001452; -.
InterPro; IPR002048; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caenorhabditis elegans.
Eukaryota; Metazoa; Nemato
Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                     investigating biology.";
Science 282:2012-2018(1998).
-!- SIMILARITY: TO EF-HAND FAMILY.
EMBL; ALI17204; CAB55138.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Y116A8C.36 PROTEIN.
Y116A8C.36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
                                                                                                                                                                                               SMART; SM00054;
Calcium-binding.
SEQUENCE 1097
                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (JAN-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9U2T9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9U2T9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                 "Genome sequence of the nematode C.elegans:
                                              687
                                                                                           627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        558
  747
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 ARSRQGSGVILRQEEAEY
                                                                     44
                       77
                                                                                                                                                    Local
                                                                                                                6
                                                                                                                                                               Match
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                                                                                                                GNFDSEERSSWY---WGRLSRQEAVA-LLQGQRH-----GVFLVRDS---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HLDENSPLGDLLGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-SVNTPLPNLQNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EGGWWRG-DCGGKKQMWFPANYMEEIFSP
 MPPNMTPSSSVDQIGVKAARKAEIAAA-----
                                            RSEDELSFEPGDVIIVFQSHAAEPGWRAGQLREKVGWFPEAFVEAIAAVPTPGGDPPIQN 746
                                                                                        GEFDKTDASQRFDADFGATSTADPFAQIAQAPAHSKGAVDQSAFNIHDTYKCRALFAFEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EEQWWNAEDSEGKRGM-IPVPYVEK-YRPASASVSALIGGNQEGSHPQPLGGPEPGPYAQ 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTPDPDYGALYEGRNPGFYVEANPMPTFKCSVRALFDYKAQREDELTFTKNTIIQNVEKQ
                    SPAQPPPGVSPSRLRIGDQEFDSLPALLEFYKIHYLDTTTLIEPVARSRQGSGVILRQEE
                                                                                                                                       75; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A . A .
                                                                   STSPGDYVLSVSENS
                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nematoda;
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21.2%;
                                                                                                                                                                                               122071 MW;
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13,
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                                                                                                                                     56;
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Last sequence update)
Last annotation update)
                                                                                                                                      Score 182; DB
Pred. No. 1.5e
56; Mismatches
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                                                                                                                                                                                              1C2BA5F103968372 CRC64;
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                                                                                                                                                                                                                                                      UNKNOWN_1
                                                                   -RVSHY----- TINSSGPRPPVPP 76
MGLTEGGAPPASSAPAAAAVISQCI 798
                                                                                                                                                  DB 5;
.5e-06;
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RESULT
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Best Local
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Pfam; PF00018; SH3; 2.
Pfam; PF002208; Sorb; 1.
PFINTS; PR00499; P67PHOX.
PRINTS; PR00451; PRICHEXTENSN.
PRINTS; PR00151; PRICHEXTENSN.
PRINTS; PR00452; SH3DOMAIN.
PROSITE; PS50002; SH3; 2.
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01-AUG-1998
01-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wang B., Golemis E.A., Kruh G.D.;
"ArgBP2, a multiple Src homology 3 domain-containing, Arg/Ab
"nteracting protein, is phosphorylated in v-Abl-transformed
localized in stress fibers and cardiocyte z-disks.";
J. Biol. Chem. 272:17542-17550(1997).
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE=97362243; PubMed=9211900;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF049885;
HSSP; P29354; 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ARG/ABL-INTERACTING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002965;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001452;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000108;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  853
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QPLGGPEPGPYAQPSVNTPLPNLQNGPIYARVIQKRVPNAYDKTALALEVGELVKVTKIN 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PNAYDKTALALEVGELVKVTKINVSGQWEGECNGKRGHFPFTHVRLLDQQNPD
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                                                                                             LPFKKGDILRIRDKPEEQWWNAEDSEGKRGMIPVPYYEKYRPASASVSALIGGNQEGSHP
                                                                                                                                                               TPEKEKLPA--
                                                                                                                                                                                            DQEFDSLPALLEFYKIHYLDTTTLIEPVARSRQGSGVILRQEEAEYVRALFDFNGNDEED
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                                                                    LSFKKGDTVYILRKIDQNWYEGE-HHGRVGIFPISYVEKLTP
                                                                                                                                                                                                                                                       SRTSPGRVDLPGSSTTLTKSF--TSSSPSSPSRAKDRESPRSYSSTLTDMGRSAPRERRG
                                                                                                                                                                                                                                                                                                   SSTSPGDYVLSVSENSRVSHYIINSSGPRPPVPPSPAQPP-----PGVSPSRLRIG
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72; Conserv
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B (TrEMBLrel.
L (TrEMBLrel.
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70660 MW;
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Primates;
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                                                                                                                                                                                                                                                                                                                                               29;
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Last sequence update)
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EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                     Score 173;
Pred. No. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                030A8C5036331674 CRC64;
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                                                                                                                                                                                                                                                                                                                                                  84;
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Best Local S
Matches 72
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InterPro: IPR003127; ...
Pfam; PF00018; S33; 3.
Pfam; PF00208; Sorb; 1.
PRINTS; PR00452; SH3DOMAIN.
PROCOM; PD016158; .; 1.
PROSITE; PS50002; SH3; 3.
SMART; SM00326; SH3; 1.
SEQUENCE 666 AA; 74803 MW; 1
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"ArgBP2, a multiple Src homology 3 domain-containing, Arg/At interacting protein, is phosphorylated in v-Abl-transformed localized in stress fibers and cardiocyte Z-disks.";
J. Biol. Chem. 272:17542-17550(1997).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                 QPLGGPEPGPYAQPSVNTPLPNLQNGPIYARVIQKRVPNAYDKTALALEVGELVKVTKIN 273
                                                                                                                                                                                                                                                                                  TPEKEKLPA
                                                     VDQNWYEGKIPGTNRQGIFPVSYVEVVKKNTKGAEDY
                                                                                         VSGQW-EGECNG--KRGHFPFTHVRLLDQQNPD-EDF 306
                                                                                                                             ----PEK---AQPA--RPPPPAQPGEI-GEAIAKYNFNADTNVELSLRKGDRVILLK-R
                                                                                                                                                                                                                                           LPFKKGDILRIRDKPEEQWWNAEDSEGKRGMIPVPYVEKYRPASASVSALIGGNQEGSHP
                                                                                                                                                                                                                                                                                                                  DQEFDSLPALLEFYKIHYLDTTTLIEPVARSRQGSGVILRQEEAEYVRALFDFNGNDEED 153
                                                                                                                                                                                                                                                                                                                                                      SRTSPGRVDLPGSSTTLTKSF--TSSSPSSPSRAKDRESPRSYSSTLTDMGRSAPRERRG
                                                                                                                                                                                                                                                                                                                                                                                          SSTSPGDYVLSVSENSRVSHYIINSSGPRPPVPPSPAQPP---
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                                                                                                                                                                                                         LSFKKGDTVYILRKIDQNWYEGE-HHGRVGIFPISYVEKLTP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----PEK---AQPA--RPPPPAQPGEI-GEAIAKYNFNADTNVELSLRKGDRVILLK-R 561
                                                                                                                                                                                                                                                                                                                                                                                                                                l Similarity
72; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                  29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 173; DB 4;
Pred. No. 4.4e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B549A26DC04782E0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         666
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on update)
                                                     573
                                                                                                                                                                                                                                                                                                                                                                                                                                  92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                          ---PGVSPSRLRIG 93
                                                                                                                                                                                                                                                                              -KAVYDFKAQTSKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                _Arg/Abl
                                                                                                                                                                                                                                                                                                                                                                                                                                84;
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                                                                                                                                                                                                                                                                                                                                                        425
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ACCOMENTATION
ACCOMENTATI
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042287
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Best Local
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DKFZP586P1422
                                                 NCBI_TaxID=8355;
                                                                   Xenopodinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-UTERUS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [nterPro;
                                                                                                                                                                                                                                                                                                                                        682
                                                                                                                                                                                                                                                                                                                                                                          274
                                                                                                                                                                                                                                                                                                                                                                                                                638
                                                                                                                                                                                                                                                                                                                                                                                                                                                  214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69;
                                                                     Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N.A.
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042287 PRELIMINARY;
042287;
01-JAN-1998 (TrEMBLrel. 05, C
01-JAN-1998 (TrEMBLrel. 05, L
01-MAR-2001 (TrEMBLrel. 16, L
INTERSECTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003127; -. Pfam; PF00018; SH3; 3. Pfam; PF000208; Sorb; 1. PRINTS; PR00499; P67PHOX. PRINTS; PR00452; SH3DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  O9UFT2 PRELIMINARY; PRT; 816 AA.
09UFT2;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
HYPOTHETICAL 90.2 KDA PROTEIN.
SEQUENCE FROM HOffman N.G.,
                                                                                Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Ven
Amphibia; Batrachia; Anura; Mesobatrachia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Koehrer K., Beyer A., Mewes
Submitted (SEP-1999) to the
EMBL; AL117472; CAB55947.1;
HSSP; Q60631; 1GBQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein. SEQUENCE 816 AA; 90201 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50002; SH3; 3
SMART; SM00459; Sorb; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VDENWYEGRIPGTSRQGIFPITYVDVIKRPLVKNP
                                                                                                                                                                                                                                                                                                                                       VSGQW-EGECNG--KRGHFPFTHVRLLDQ----QNP
                                                                                                                                                                                                                                                                                                                                                                                                         QPLGGPEPGPYAQPSVNTPLPNLQNGPIYARVIQKRVPNAYDKTALALEVGELVKVTKIN
                                                                                                                                                                                                                                                                                                                                                                                                                                           LPLQKGDIVYIYKQIDQNWYEGE-HHGRVGIFPRTYIELLPPAEK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LPFKKGDILRIRDKPEEQWWNAEDSEGKRGMIPVPYVEKYRPASASVSALIGGNQEGSHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESDGAPGD--LTSLENERQIYKSVLEGGDIPLQGLSGLKRPSSSASTKDSESPR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DQEFDSLPALLEFYKIHYLDTTTLIEPVARSRQGSGVILRQEEAEYVRALFDFNGNDEED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ····-HFIPADYLEST···EEFIRRHD····-DKEMRPARAKFDFKAQTLKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
N.A.
Hardison
                                                                                                                                                                                                                                                                                                                                                                           -AQPKKLTPVQVLE----YGEAIAKFNFNGDTQVEMSFRKGERITLLR-Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.8%;
25.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mewes
to the
 N.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34;
                                                                                                                                                 Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    H.W., Gassenhuber
EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 170; DB 4; Pred. No. 1e-05;
 Yamabhai M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FFFE6647DC7730D4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches 100;
                                                                                                                                                                                                                         1270
                                                                                                  Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                          716
                                                                                                                                                                                                                                                                                                                                        302
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 Kay
                                                                                  Pipoidea; Pipidae;
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                                                                                                                                                   update)
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databases.
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                                                                                                                                                                                                                                                                                                                                                                           681
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RESULT
035413
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 75
InterPro; IPR000452; ...
InterPro; IPR001452; ...
InterPro; IPR003127; ...
Pfam; PF00018; SH3; 3.
Pfam; PF02208; Sorb; 1.
PRINTS; PR00452; SH3DOMAIN.
PRODUM; PD016158; ...
PRODUM; PS0002; SH3; 3.
PROSITE; PS00028; ZINC_FINGER_C2H2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001452; -.
InterPro; IPR002048; -.
Pfam; PP00018; SH3; 5.
Pfam; PF00036; efhand; 2.
PRINTS; PR00452; SH3DOMAIN.
PROSITE; PS00018; EF_HAND; UNKNOWN_2.
PROSITE; PS00027; EH; 1.
SMART; SM00027; EH; 1.
                                                                                                                                                                                                                  Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                       01-JAN-1998 (TrEMBLrel. 05, Created)
01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
SH3-CONTAINING PROTEIN P4015.
                                                                                                                      Ide N. Takeuchi M., Hata Y., Takai Y.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ
EMBL; AF026505; AAB81527.1; -
HSSP, P29354; IGRI.
                                                                                                                                                                                                                                                                                                                             035413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1040
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SPONENCE 1270 AA; 143670 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.

-:- SIMILARITY: TO EF-HAND FAMILY.

EMBL; AF0322118; AAC73068.1; -.

HSSP; P29355; 1SEM.
                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                035413;
                                                                                                                                                                                                                                                                                                                                                                                                1126
                                                                                                                                                                                                      NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000261; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 EERSSWYWGRLSRQEAVALLQGQRHGVFLVRDSSTSPGDYVLSVSENSRVSHYIINSSGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
nes 75; Conserv
                                                                                                                                                                                                                                                                                                                                                       13
                                                                                                                                                                                                                                                                                                                                                                                               KSTPTE 1131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PNAYDKTA---LALEVGELVKVTKINVSGQWEGE--CNGKR---GHFPFTHVRLL----D
                                                                                                                                                                                                                                                                                                                                                                                                                                               --SYAATAPEQLTLAPGQLILIRKKNPGGWWEGELQARGKKRQIGWFPANYVKLLSPGTN 1125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EKYRPASASVSALIGGNQEGSHPQPLGGPEPGPYAQPSVNTPLPNLQNGPIYARVIQKRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----EYI-SMYTYESNEQGDLTFQQGDLT-VVIKKDGDWWTGTVGE-KTGVFPSNYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EQQDMWWFGE - -
                                                                                                                                                                                                                                                                                                                                                                                                                       QQNPDE 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ILRQEEAEYVRALFDFNGNDEEDLPFKKGDILRIRDKPEEQWWNAEDSEGKRGMIPVPYV 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RPPVPPSPAQPPPGVSPSRLRIGDQEFDSLPALLEFYKIHYLDTTTLIEPVARSRQGSGV 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -RPKDSEAAG--SGGKTGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----ASLKRVSSPAFK--PAI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 165; DB 13,
Pred. No. 4.7e-05;
Prematches 79;
                                                                                                                                                                                                                 Craniata; Vertebrata;
Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EA940C1F6B6A6858 CRC64;
                                                                                                                                                                                                                                                                                                                             1196
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                                                                                                                                                    databases
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                                                                                                                                                                                                                 Euteleostomi;
;; Murinae; Rat
                                                                                                                                                                                                                    Rattus
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Qγ
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Q9P7E8
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SQ
                                                                                                                                                  Query Match
Best Local S
Matches 57
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Best Local Similarity
Matches 57; Conserv
                                                                                                                                                                                                                                                                                                                         Harris D., Wood V., Rajandream M.A., B. Submitted (MAR-2000) to the EMBL/GenBau EMBL, AL162631; CAB83085.1; -. InterPro; IPR000108; -. InterPro; IPR0001452; -. InterPro; IPR002108; -. InterPro; IPR002108; -. InterPro; IPR00255; -.
                                                                                                                                                                                                                  Pfam; PF00018; SH3; 2.
Pfam; PF00241; Cofilin_ADF; 1.
PRANTS; PR0049; P67PHOX.
PRINTS; PR01217; PRICHEXTENSN.
PRINTS; PR00452; SH3DOMAIN.
PROSITE; PS50002; SH3; 2.
SMART; SM00102; ADF; 1.
SEQUENCE 857 AA; 91137 MW; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O997E8 PRELIMINARY;
O997E8,
O997E8,
O997E8,
O1-OCT-2000 (TIEMBLrel. 15, Created)
O1-OCT-2000 (TIEMBLrel. 15, Last sequence update)
O1-MAR-2001 (TIEMBLRel. 16, Last annotation update)
ACTIN BINDING PROTEIN WITH SH3 DOMAINS.
SPAPJ760.O2C.
SPAPJ760.O2C.
Schizosaccharomyces pombe (Fission yeast).
Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1030
                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-972H-;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schizosaccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00326; SH3; SEQUENCE 1196 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=4896
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
180 GKRGMIPVPYVEKYRPASASVSALIGGNQEGSHPQPLGGPEPGPYAQPSVMTPLPNLQNG | ::|: | | :| | | :| |
                                           712
                                                                    124
                                                                                               663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      292
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                                                                                                                          68
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                                        --QVGGDVKATEHTQPTKTPAIVIYDYSPEEENEIELVENEQIQILEFVDDGWWLGENSK
                                                        SRQGSGVILRQEEAEYVR----ALFDFNGNDEEDLPFKKGDILRIRDKPEEQWWNAEDSE
                                                                                                                       SGPRPP----VPPSPAQPPPGVSPSRLRIGDQEFDSLPALLEFYKIHYLDTTTLIEPVAR 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PVQPGEI-GEAIAKYNFNADTNVELSLRKGDRIILLK-RVDQNWYEGKIPGTNRQGIFPV
                                                                                             SVPQPPAAPVVPEVPSVPQPPAVPVVPEAGQLNEPVVPPLPPH-----DETQ--EP---
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57; Conser
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134052 MW;
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Pred. No. 5.3e-05;
1; Mismatches 70;
                                                                                                                                                 Score 163.5; DB 3; Pred. No. 3.7e-05; 5; Mismatches 87;
                                                                                                                                                                                                                     247EFA78BAFE7097
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RN [1]
RR SEQUEN
RC TISSUE
RA Lin W.
RL SUBMIT
DR HSSP;
DR INterP
DR Ffam;
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C TISSUE-LLVER;

A Lin W.S. (Chuang L.M.;

A Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.

R EMBL; AF136380; AAD27647.1; -.

R HSSP; Q66631; 1GBO,

R InterPro; IPR00108; -.

InterPro; IPR001452; -.

R InterPro; IPR003127; -.

R InterPro; IPR003127; -.

R Ffam; PF00218; SH3; 3.

Pfam; PF00218; SH3; 3.

R Pfam; PF02208; Sor1; 1.

R PRINTS; PR00452; SH3DOWAIN.

R PRINTS; PR00452; SH3DOWAIN.

R PRINTS; PS00020; SH3; 3.

R PRSTITE; PS50002; SH3; 3.

R SMARR; SM00315; SH3; 1.

SMARR; SM00326 SH3; 1.

SMARR; SM00326 G84 AA; 76341 MW; 2274E632BB07329C CRC64;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
SH3P12 PROTEIN.
HOMO Sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                            GECNG--KRGHFPFTHVRLLDQ---QNP 302
                                                                                                                                                                                                                                                                                                                                                                               PGPYAQPSVNTPLPNLQNGPIYARVIQKRVPNAYDKTALALEVGELVKVTKINVSGQW-E 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PA-----DYLEST---EEFIRRRHD------DKEMRPARAKFDFKAQTLKELPLQKGD 468
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